

**FIG. 1**

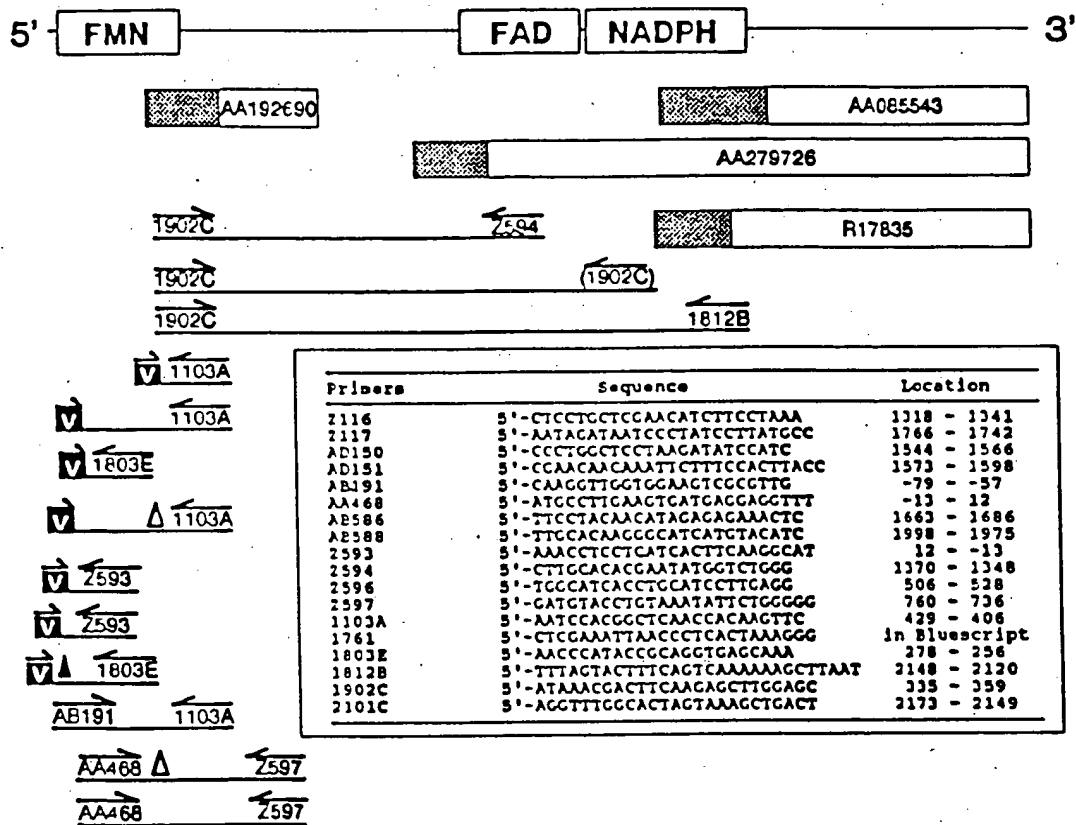


FIG. 2



CAAGCTTGGTGGAGTCTGCTGTCAGGTTCCTGCCGGCTGGCGGGCTGGTTCCTGCTTACATCGCTTGAAGT

1 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAAGCCATCGCAGAAGAAATGTGTGAGCAAGCTGTGGTACATGGATTTCCTGCAAGTCTTCAGTGTATTAGTGAA  
M R R F L L L Y A T O G Q A K A I A E E M C E Q A V V H G F S A D L H C I S E 40

121 TCCGATAAGTATGACCTAAACCGAACAGACTCTCTGTGTGTGTCTTACCACGGGACCGGAGACCCACCGACACACCGCCGCAAGTTTGTTAAGGAATAACAGAACCAACA  
S D K Y D L K T E T A P L V V V S T T G T G D P P D T A R K F V K E I O N Q T 80

261 CTGCCGGTGTGATTCCTTGTCTCACTCGCGGTATGGGTACTGGGTCTCGGTGATTGAGATACACCTACTTTGCAATGGGGGAAGATAATTGATAACGACTTCAAGAGCTTGGAGCC  
L P V D F F A H L R Y G L L G L G D S E Y T Y F C N G G K I I D K R L Q E L G A 120

361 CGGCATTCTATGACACTGGACATGCAAGTACTGTAGGTTAGAACTGTGGTGTGACCGTGGATTCTGGACTCTGGCAGCCCTCAGAAAGCAATTTAGGTCAAGCAGGACGACAA  
R H F Y D T G H A D D C V G L E L V V E P W I A G L W P A L R K H F R S S R G O 160

481 GAGGAGATAAGTGGCGCACTCCCGGTGGCATCACCTGATCTCTGGAGCAGACCTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCGAGCTCTCTGAGATTGCGATTCAGGA  
E E I S G A L P V A S P A S L R T D L V K S E L L H I E S O V E L L R F D D S G 200

601 AGAAAGGATTCTGAGGTTTTGAACCAAAATCGATGACCAAGCAACCAATCCAAATGTTGTAATTAAGACACTTTGAGTCTCACTTACCGTTCGCTTACCGTTCGCTTCAACAGCTCTCA  
R K D S E V L K Q N A V N S N O S N V V I E D F E S S L T R S V P P L S O A S L 240

721 AATATTCTGGTTTACCCCGCAGATATTTACAGGTACATCTGCGCAGGACTCTTGGCCAGGAGCAAGCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCCAATTTCAAG  
N I P G L P P E Y L Q V H L Q E S L G Q E E S O V S V T S A D P V F O V P I S K 280

841 GCAGTTCAACTTACTACGAATGATGCCATAAAACCACCTCTGCTGGTAGAATTGGACATTTCAATACAGACTTTTCTATCAGCTGGAGATGCTTCAGGGTGATCTGCCCTAACAGT  
A V O L T T N D A I K T T L L V E L D I S N T D F S Y O P G D A F S V I C P N S 320

961 GATTCTGAGGTACAAAGCCCTACTCCAAGACTGCAGCTTGAGATAAAGAGAGCACTGGCTCCTTTTGAATAAAGGAGACACAAAGAAAGAAAGAGTACCTTACCCAGCATATA  
D S E V Q S L L O R L O L E D K R E H C V L L K I K A D T K K G A T L P O H I 360

1081 CCTCGGGATGTTCTCTCCAGTTCATTTTACCTGGTGTCTGAAATCCGAGCAATTTCTAAAGGCAATTTTTCGAGCCCTTGTGGACATATACAGTGACAGTCTGAAAAGCGCAGG  
P A G C S L O F I F T W C L E I R A I P K K A F L R A L V D Y T S D S A E K R R 400

1201 CTACAGGAGCTGTGAGTAAACAGGGGCGAGCGGATATAGCCGCTTTGTAGAGATGCTGTGCTCTGCTGCTTGGATCTCTCTGCTTCCCTTCTTGGCAGCCACCACTCAGTCTC  
L Q E L C S K O G A A D Y S R F V R D A C A C L L D L L A F P S C O P P L S L 440

1321 CTGCTCGAATCTCTCTAAACTTCAACCCAGCACCATATTCTGTGCAAGCTCAAGTTTATTCACCAGAAAGCTCCATTTTGCTTCAACATTGTGGAATTTCTGTCTACTGCCACA  
L L E H L P K L O P R P Y S C A S S L F H P G K L H F V F N I V E F L S T A T 480

1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGCTGGCTGGCTGTGTTGCTTCAGTCTTCAGCCAAACATACATGCATCCATGAAGACAGCGGGAAGCCCTGGCTCTCAAGATA  
T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I 520

1561 TCCATCTCTCGAACACAAATTTCTTCCACTTACCAGATGACCCCTCAATCCCATCAATAATGGTGGTCCAGAACCGGATAGCCCGCTTATTTGGGTTCCTACAAATAGAGAG  
S I S P R T T N S F H L P D D P S I P I I M V G P G T G I A P F I G F L Q H R E 560

1681 AAACCTCCAAGAACACCCAGATGGAAATTTTGAGCAATGTGGTGTGTTTGGCTGCAGCATAGGATAGGATATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGCATGGG  
K L O E O H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G 600

1801 ATCTTAACATCTAAAGGTTTCTCTCTCAAGAGATGCTCTGTGTTGGGAGGAGGAGGCCCAAGCAAGTATGTACAAGACACATCCAGCTTTCATGGCCAGCAGGTGGCGAATCCTC  
I L T H L K V S F S R D A P V G E E A P A K Y V O D N I O L H G O O V A R I L 640

1921 CTCAGGAGACGGCCATATTTATGTGTGCGAGATGCAAGATATGCCAAGGATGATACATGATGCCCTTGTGCAATAAAGCAAGAGGTGGAGTTGAAACATAGAACCAATG  
L Q E N G H I Y V C G D A K N M A K D V H D A L V O I I S K E V G V E K L E A M 680

2041 AAAACCTGGCCACTTTAAAGAGAGAAAACGCTACCTTCAGGATATTTGGTCTATAAACACCAAGAAATTAAGAAAGGATTAAAGCTTTTGTGACTGAAAGTAAAGTACAGCTTTAC  
K T L A T L K E E K R Y L O D I W S \*\*\* 698

2161 TAGTGCCAAACCTTTAAATTTTCAACAAATTTTCTTCAACATTTCTTGAAGGACATGGAGTGGATTCATTTAACAAATCTCCTGATTTGATTTTACGATATC  
2281 TTCATCTACGCCCTTCTGCTGCTGACTCTCCCAATTTGCCCTGTGCTTGAGCTTCTGAGCTTAAGCGAGCTCTCAGTCCCTATCAGAGCTCTTACTTCTCCAGAACT  
2401 TCACAGAGCTGTCTCTCCATCGAAATAGGAGGACTGACTGAGTGGCTCATCTTGTGACTACAGTGCACATTTAAAGAGTATGAAAGATGATAAATTTATTTA  
2521 ATAAATATACCCATAAAGATCTCATATTAATGACTTAATTTACATGACTAGACATATCTGTATGTATTGTAACATCAATGATTTTGTACTAAGCTATATTTCTG  
2641 ATAGAAATTTTAGAATAATGCTCATAGGATTTTATTTATGATGCTGGGAAATAGAAATGATTTTAAATTTTCACTCTGGCATATGGATTATCTATCACTACTCTT  
2761 TTTAAGTCACAATTTGAGCAATTTGGGCAATTTGCATTCATTTACAGCTACGATGCTGATCATTTTAAATAGANAGATACACCTTTTATTTTCACTCTTTTATTTCTGCTCTT  
2881 GGCACATTTTGTAGTTTCCACATTTTGTCCATCATACCCTCAAGCAGTGTGCTGGAATTAAGTCTGATCTGGAATTTTACGATTTTCCAGTCTCCAGTCTGCTGCTAAT  
3001 TCCCTGTTAATTTGCACACAAACAAATTTATGATAATCTTCTCCACTGTCTTATATATATGTTATTTATGATGCTTGGGATTTAAACATCTCTGTTGAAGGCTTT  
3121 TGAATCTTTTGAAGAAATTAAGATCTGAAGAAATGGCAATATCTTAAACAAAAAATAAAAAA

HsMTRR	.....	
CeMTRR	.....	
HsCPR	MGCSHVDTSSTVSEAVAEVSLFSMTDHLFSLIVGLLTIVFLFRKKKEE	50
HsMTRR	.....FMN.....	24
CeMTRR	.....MRRFLLLTATCCGCAKIAEENCE	24
HsCPR	VFEFTKIGTLTSSVRESSFVEKMKKTGRNIIVFYCSOTGTAEEFANRLSK	100
HsMTRR	.....FMN.....	66
CeMTRR	CAVVVCFSAHLHCISESDK-YDLKT-----ETAPLVVVSTTGTGDP	66
HsCPR	KAELIGLTFRLHALCENEKKFHLNE-----EKLC-AIVVSTGGDAP	66
	DANRYG----MRGMSADPEEYDLADLSSLEIDHALVVFCHATYCEGOPT	146
HsMTRR	.....FMN.....	116
CeMTRR	CTARFVKETCNCTLPVDFFAHLRTGLLGLGDSYTYFCNGGKIIDKRLQ	116
HsCPR	ENCAFFVERINRNSLENEYLNLDYVLLGLGDSYSSYGTIFRKIDKOLT	116
	DNACDFYDLGCTGDV---LSGVKFAVFLGNKTYENFANGKYVOKRLE	193
HsMTRR	ELGARNFYDICHADDCVGLLEVPEVIAGLVFAIRKHFSSRGCEEISGA	166
CeMTRR	ALGARNLFGRAEADDCVGLLEVPEVIAGLVFAIRKHFSSRGCEEISGA	162
HsCPR	OLGACIFELGLGDDGNLEEDFITWRECFWFAVCENF-----GV	233
HsMTRR	LFVASPAELRTDLVKSELLNIESOVELL--RFDCSGRKDSEVLKNAVNS	214
CeMTRR	-AITESSNLKNCVKTE---EKKALLCKRIEDEESDDEGRGVIGID-	206
HsCPR	EATGEESIKCTEL-----VVHTDIAAKVYNGEMGRKSYEN	271
HsMTRR	NCENVVIEDF---EESLTRSVPLS-CASLWIPGLPPETLQVHLCESLGQ	260
CeMTRR	---MLIFEHTDYPEISLLKGSOTLSHDEHLRVPJAPCPFIYSSVSFKLP	253
HsCPR	CKP-----FID-----AKNPFLAAVTINRKLN	293
HsMTRR	EESCVS-----VTSADPVFCVPISKAVOLT--NDAIKTLLVELDIS	301
CeMTRR	EDTXLEWNLCKNFCVVTXFFEVLVSAEFVTDPSKKIKTKRMITVDFG	303
HsCPR	GGTE-----FNLHLELD	306
HsMTRR	N--TDFSTYCGDAFSVICPNSDSEVCSLLGR-LOLEDKREHCVLLKIKAD	348
CeMTRR	ENAAELCTEFCDAITYCVNPALEVNFIKRCGVLDIADOCCEL-SINPK	352
HsCPR	ISCSKIRYESGDHVAVYPANDSALYNOLCK---ILGADLD--VMSLHNL	351
HsMTRR	TKKKGATLPCNIPACCSLOFIFTWGLEIRAIKKAFLRALVDYTSDAEK	398
CeMTRR	TEKINACIFCHVHKITTLRHMTTCLDIRAPGRPLIRVLAESTDSFHEK	402
HsCPR	DEESKXMF--IFCPTSYRTALTYTLDITNPPRTNVLTELACTASEFSEQ	399
HsMTRR	RPLOEL--CSKCGAACYSRFRVDAACALLDILLAFSPCOPPLSLLLEMLP	446
CeMTRR	FRILLEL--CSACGMDFTDFVTPGLSLADMLFATPNVKKPPVORLIELLP	450
HsCPR	ELLKKNASSSGCKELYLSVVVEARRHILAILDCCPSLRPPIDHLCCELLP	449
HsMTRR	.....FAD.....FAD.....FAD.....	496
CeMTRR	RLCPRTYSCASSSLFHFGKLFHVFNIVEFLSTATTEVLRKGVCTGWLALL	497
HsCPR	RLCPRTYSSSS--YENRKRLITYSENEFPATGGRHSRKLATDULNSL	496
	RLCARTYSIASSSKVHPNSVNICAVVETETKAGR--INKGVATNUL---	496
HsMTRR	VASVLOPNINASHEDSGKALPKISISPRTTNSFNLP-----DDPSIP	539
CeMTRR	R-----IGDKVVLGKEFARFRLPPLGHTKNSACKLP	529
HsCPR	RAKE-----FVGENCGRALVPHFVKSOFRLPFK-----ATT	527
HsMTRR	.....NADPH.....	588
CeMTRR	ITMVCPGTCTIAFFIGFLOHREKLOEGHPDGNFGAMW-LFFGCRNKKDRYL	579
HsCPR	LLMVCPGTGVSVFLSFLHFLRLKQDPSDFVDVPRVLFPGCRDSSVDAI	574
	VIMVCPGTGVAFFIGFIOERAWLRGOGKE---VGETLLTYGCRSDEDYL	574
HsMTRR	.....NADPH.....NADPH.....	638
CeMTRR	FRKELRHFLKNCILTNLKVFSRDAFVGEESAFKTYVDNIOLNGCOVAR	621
HsCPR	YHSELEHFVSEGITDILICESEQ-----XGERVODGLRKYLDKVLP	618
	YREELAGFHRDGLTOLNVAFSRE-----GSHKVYVCHLLKQOREHLWK	618
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CeMTRR	ILLQE-NGHITYVCGDAKNHAKDVHDALVOTISKEVGVKLEAMKTLATLK	671
HsCPR	FLTASTESKIFICGDAKNSKDVVQCFSDIVASDGIPOLEAKKLNOLK	666
	LI--EGGAHITYVCGDARNHARDVONTFYDIAELGAMENAGAVDYIKKLM	666
HsMTRR	.....NADPH/FAD.....	698
CeMTRR	EEKRTLODIWS	682
HsCPR	KSDQYIEDVWG	677
	TKCRYSLDVWS	677

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HsMTRR	-----	
CeMTRR	-----	
HsCPR	MGGLVDTSSVTSEAAVEVSLFSMTDMILFSLIVGLLTYWFLPKKKEL	50
	FMN	
HsMTRR	-----MRRFLLLYATOGGAIAEEMCE	24
CeMTRR	-----MTDFLIAFGSQTGOAETIAKSLKE	24
HsCPR	VPEFTKIOTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSK	100
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	FMN	
HsMTRR	OAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVSTTGTGDP	66
CeMTRR	KAELIGLTPRLHALDENEKKFNLE-----EKLC-AIVVSTGDDGAP	66
HsCPR	DAHRYG---MRGMSADPEYDLADLSSLPEIDNALVVFCMATYGEDPT	146
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	FMN	
HsMTRR	DTARKFVKEIQNQLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ	116
CeMTRR	DNCARFVRRINRNSELENYLKNLDYVLLGLGDSNYSSYOTIPRKIDKOLT	116
HsCPR	DNAODFYDWLOETDVD---LSGVKFAVFGNGKTYEHFAMGKYVDKRL	193
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HsMTRR	ELGARHFYDTGHADDCVGLLVVEPWIAGLWPALRKHFSSRGEEISGA	166
CeMTRR	ALGANLFDRAEADDOVGLELEVEPWIEKFATLASRFDISADKMN----	162
HsCPR	OLGAORIFELGLGDDGNLEEDFITVREQFWPAVCEHF-----GV	233
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HsMTRR	LPVASPASLRDVLKSELLHIESOVELL--RFDDSGRKDSEVLKONAVNS	214
CeMTRR	-AITESSNLKNOVKTE---EEKKALLOKRIEDEESDDEGRGRVIGID-	206
HsCPR	EATGEESSIROYEL-----VVHTDIDAAKVYMGEMGRKLSYEN	271
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HsMTRR	NCSNVVIEDF---EESLTSVPPLS-QASLNIPGLPPEYLOVHLOESLGO	260
CeMTRR	---MLIPEHYDYPEISLLKGSOTLSNDENLRVPIAPQPFIVSSVSNRKLP	253
HsCPR	OKP-----PFD-----AKNPFLAAVTINRKLN	293
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HsMTRR	EESQVS-----VTSADPVFQVPISKAVOLTY--NDAIKTLLVELDIS	301
CeMTRR	EDTKLEWNLCKMPGVVTKPFEVLVSAEFVTDPFSSKIKTKRMITVDFG	303
HsCPR	OGTE-----RHLMHLELD	306
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HsMTRR	N--TDFSYPGDAFSVICPNSDSEVQSLLQR-LQLEDKREHCVLLKIKAD	348
CeMTRR	DHAAELOEYEPGDAIYFCVPNPALEVNFIKRCGVLDIADOOCEL-SINPK	352
HsCPR	ISDSKIRYESGDHVAVYPANDSALVNOLGK---ILGADLD--VMSLNHL	351
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HsMTRR	TKKKGATLPQHIPAGCSLOFIFTWCLEIRAIPKKAFLRALVDYTSDSA	398
CeMTRR	TEKINAQIPGHVHKITTLRHMFTICLDIRRAPGRPLIRVLAESTSDPNEK	402
HsCPR	DEESNKKHP--FPCPTSYRTALTYLDITNPRTNVLYELAQYASEPSEQ	399
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HsMTRR	RRLOEL--CSKOGAADYSRFVRDACACLDLLAFSPCOPPLSLLLEHLP	446
CeMTRR	RRLLEL--CSAOGMKDFIDFVRTPGLSLADMLFAFPNVKPPVDRLIELLP	450
HsCPR	ELLRKMASSSGEGKELYLSWVEARRHILAILQDCPSLRPPIDHLCCELL	449
	*.*.*.*.*	
	FAD	
HsMTRR	KLOPRPYSCASSSLFHPGKLHFVFNIVEFLSTATTEVLRKGVCTGLWALL	496
CeMTRR	RLIPRPYSMS--YENRKARLIYSEMEFPATDGRHRSRKLATDWLNSL	497
HsCPR	RLOARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---	494
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HsMTRR	VASVLOPNIHASHEDSGKALAPKISISPRTTNSFHLP-----DDPSIP	539
CeMTRR	R-----IGDKVOVLGKEPARFRLPPLGMTKNSACKLP	529
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFK-----ATTP	527
	*.*.*.*.*	
	NADPH	
HsMTRR	IIMVGPGTGIAPFIFGLQHREKLOEHPDGNFGAMW-LFFGCRHKORDYL	588
CeMTRR	LLMVGPGTGVSVFLSFLHFLRKLDKODSPSDFVDVPRVLFVGGCRSSVDAI	579
HsCPR	VIMVGPGTGVAPFIFGIERAWLROOGKE---VGETLLYYGCRSSDEDYL	574
	*****..*.*.*	
	NADPH	
HsMTRR	FRKELRHFLKHGILTHLKVFSRDPVGEAAKPYQDNIOQLHGOOVAR	638
CeMTRR	YHSELEMFVSEGIITDLIICESEQ-----KGERVODGLRKYLDKVL	621
HsCPR	YREELAQFHRDGAALTOLNVAFSRE-----QSHKVYVOHLLKGDREHLWK	618
	*.*.*.*.*	
	NADPH	
HsMTRR	ILLOE-NGHYVCGDAKNMAKDHDALVOIISKEVGVKLEAMKTATLK	687
CeMTRR	FLTASTESKIFICGDAKMSKDVWOCFSDIVASDOGIPDLEAKKLMOLK	671
HsCPR	LI--EGGAHIYVCGDARNMARDVONTFYDIAELGAMEHAQAVDYIKKLM	666
	*.*.*.*.*	
	NADPH/FAD	
HsMTRR	EEKRYLODIWS	698
CeMTRR	KSDQYIEDVWG	682
HsCPR	TKGRYSLDWS	677
	*.*.*.*	

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FIG. 5A

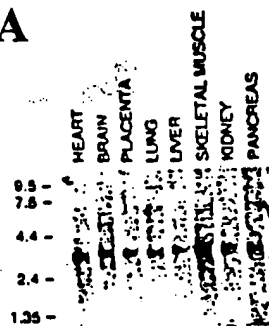


FIG. 5B



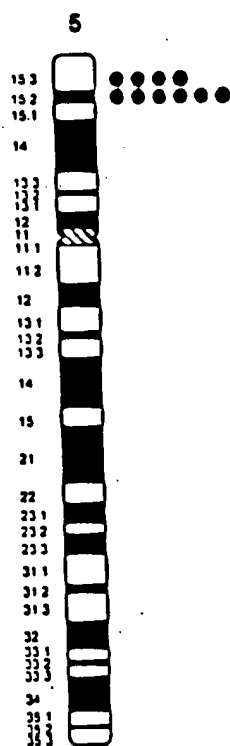


FIG. 6



FIG. 7A

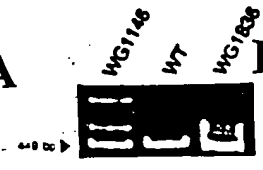


FIG. 7B

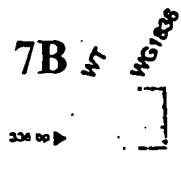


FIG. 7C

Position	Sequence	Accession/ Protein	Organism
572	CAHLLVCCWHPDHYLP	(AF025794)	MTB
558	CTLLVYCCPPSDIDLY	(AA0557)	CPR
559	CTLLVYCCPPRAEDLY	(D00101)	CPR
560	CELLVYCCPPRAEDLY	(P31090)	CPR
572	CPALLVCCWHPDHYLP	(P31114)	CPR
573	CPVLLVYCCPPSDIDLY	(Z24438)	CPR
1281	CPHLLVYCCPPSDIDLY	(D14408)	CPR
1009	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
1040	TPHLLVYCCPPSDIDLY	(U05410)	NOS 1
1009	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
1040	TPHLLVYCCPPSDIDLY	(U05410)	NOS 1
1009	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
1040	TPHLLVYCCPPSDIDLY	(U05410)	NOS 1
481	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
915	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
407	CPHLLVYCCPPSDIDLY	(U05410)	NOS 1
341	CLAVLLVYCCPPSDIDLY	(X72419)	FNR
341	CLAVLLVYCCPPSDIDLY	(P00455)	FNR

FIG. 8A

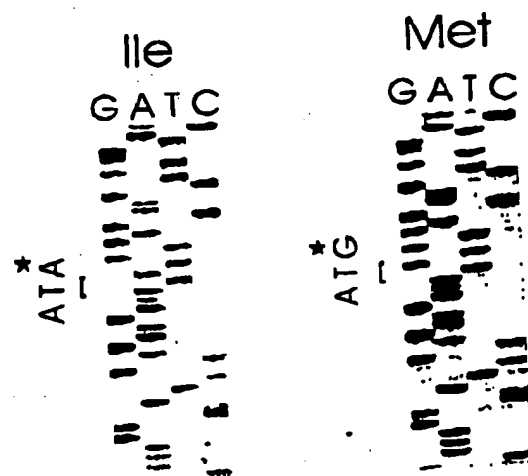


FIG. 8B

